



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/623,854
Source: OIPF
Date Processed by STIC: 8/1/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/623,854

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent wrapping.
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

see item 4 on Env summary
sheet

10/6/23, 854 1

□y"z-n•\□z delete
SEQUENCE LISTING

<110> NARA INSTITUTE OF SCIENCE AND TECHNOLOGY

<120> Multiple use of caffeine biosynthetic genes

<130> 19-023

<140>

<141>

<150> JP 2002-213655

<151> 2002-07-23

<160> 9

<170> Microsoft Word

<210> 1

<211> 372

<212> PRT

← insert this MANDATORY numeric identifier
AND its response

<300>

<301> Ogawa, M., Herai, Y., Koizumi, N., Kusano, T., and Sano, H.

<302> 7-Methylxanthine Methyltransferase of Coffee Plants. Gene Isolation and Enzymatic Properties.

<303> Journal of Biological Chemistry

<304> 276

<305> 11

<306> 8213-8218

<307> 2001-03-16

<308> BAB39215

<309> 2000-09-11

<400> 1-

Met Glu Leu Gln Glu Val Leu Arg Met Asn Gly Gly Glu Gly
1 5 10

Asp Thr Ser Tyr Ala Lys Asn Ser Ala Tyr Asn Gln Leu Val
15 20 25

Leu Ala Lys Val Lys Pro Val Leu Glu Gln Cys Val Arg Glu

Leu Leu Arg Ala Asn Leu Pro Asn Ile Asn Lys Cys Ile Lys

Val Ala Asp Leu Gly Cys Ala Ser Gly Pro Asn Thr Leu Leu

Thr Val Arg Asp Ile Val Gln Ser Ile Asp Lys Val Gly Gln

Glu Lys Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln Ile Phe

Leu Asn Asp Leu Phe Pro Asn Asp Phe Asn Ser Val Phe Lys

Leu Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly

Arg Lys Ile Gly Ser Cys Leu Ile Gly Ala Met Pro Gly Ser

These three
pages show
sample of
global errors

This file
could not be
processed -
invalid
format

Does Not Comply
Corrected Diskette Needed

delete
14 invalid
28 numbering
42
56 Per 1.822 of
70 sequence rules,
84 number the
98 amino acids
112 under every 5
126 amino acids.
140 Do NOT use TAB codes
between amino acid
numbers. Use space
characters.

Please
re-number
amino
acids

10/6/23, 854 2

Phe Tyr Ser Arg Leu Phe Pro Glu Glu Ser Met His Phe Leu
His Ser Cys Tyr Cys Leu Gln Trp Leu Ser Gln Val Pro Ser
Gly Leu Val Thr Glu Leu Gly Ile Ser Thr Asn Lys Gly Ser
Ile Tyr Ser Ser Lys Ala Ser Arg Leu Pro Val Gln Lys Ala
Tyr Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe Leu Arg
Ile His Ser Glu Glu Leu Phe Ser His Gly Arg Met Leu Leu
Thr Cys Ile Cys Lys Gly Val Glu Leu Asp Ala Arg Asn Ala
Ile Asp Leu Leu Glu Met Ala Ile Asn Asp Leu Val Val Glu
Gly His Leu Glu Glu Lys Leu Asp Ser Phe Asn Leu Pro
Val Tyr Ile Pro Ser Ala Glu Glu Val Lys Cys Ile Val Glu
Glu Glu Gly Ser Phe Glu Ile Leu Tyr Leu Glu Thr Phe Lys
Val Leu Tyr Asp Ala Gly Phe Ser Ile Asp Asp Glu His Ile
Lys Ala Glu Tyr Val Ala Ser Ser Val Arg Ala Val Tyr Glu
Pro Ile Leu Ala Ser His Phe Gly Glu Ala Ile Ile Pro Asp
Ile Phe His Arg Phe Ala Lys His Ala Ala Lys Val Leu Pro
Leu Gly Lys Gly Phe Tyr Asn Asn Leu Ile Ile Ser Leu Ala
Lys Lys Pro Glu Lys Ser Asp Val

~~154~~

~~168~~

~~182~~

~~196~~

~~210~~

~~224~~

~~238~~

~~252~~

~~266~~

~~280~~

~~294~~

~~308~~

~~322~~

~~336~~

~~350~~

~~364~~

~~372~~

<210> 2

<211> 1316

<212> DNA

<213> Coffea arabica

<220> *delete this (please delete ALL instances of this format marker throughout Sequence Listing)*

<221> CDS

<222> (45)□c(1163)

<300>

<308> AB048793

<309> 2000-09-11

<400> 2

ctttggcagt cccaaatttga tttatgtaca agtcctgcat atgaatggag 50
ctccaagaag tcctgcggat gaatggaggc gaaggcgata caagctacgc 100
caagaattca gcctacaatc aactggttct cgccaagggtg aaacctgtcc 150
ttgaacaatg cgtacggaa ttgttgcgaa ccaacttgcc caacatcaac 200

10/6/23, 854 3

<210> 4
<211> ~~C~~ mandatory response needed

<212> PRT

<213> Coffea arabica

<400> 4

Met Glu Leu Gln Glu Val Leu His Met Asn Glu Gly Glu Gly
Asp Thr Ser Tyr Ala Lys Asn Ala Ser Tyr Asn Leu Ala Leu
Ala Lys Val Lys Pro Phe Leu Glu Gln Cys Ile Arg Glu Leu
Leu Arg Ala Asn Leu Pro Asn Ile Asn Lys Cys Ile Lys Val
Ala Asp Leu Gly Cys Ala Ser Gly Pro Asn Thr Leu Leu Thr
Val Arg Asp Ile Val Gln Ser Ile Asp Lys Val Gly Gln Glu
Glu Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln Ile Phe Leu
Asn Asp Leu Phe Gln Asn Asp Phe Asn Ser Val Phe Lys Leu
Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly Arg
Lys Ile Gly Ser Cys Leu Ile Ser Ala Met Pro Gly Ser Phe
Tyr Gly Arg Leu Phe Pro Glu Glu Ser Met His Phe Leu His
Ser Cys Tyr Ser Val His Trp Leu Ser Gln Val Pro Ser Gly
Leu Val Ile Glu Leu Gly Ile Gly Ala Asn Lys Gly Ser Ile
Tyr Ser Ser Lys Ala Ser Arg Pro Pro Val Gln Lys Ala Tyr
Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe Leu Arg Ile
His Ser Lys Glu Leu Phe Ser Arg Gly Arg Met Leu Leu Thr
Cys Ile Cys Lys Val Asp Glu Tyr Asp Glu Pro Asn Pro Leu
Asp Leu Leu Asp Met Ala Ile Asn Asp Leu Ile Val Glu Gly
His Leu Glu Glu Lys Leu Ala Ser Phe Asn Leu Pro Phe
Phe Thr Pro Ser Ala Glu Glu Val Lys Cys Ile Val Glu Glu
Glu Gly Ser Phe Glu Ile Leu Tyr Leu Glu Thr Phe Lys Ala
His Tyr Asp Ala Gly Phe Ser Ile Asp Asp Asp Tyr Pro Val
Arg Ser His Phe Gln Val Tyr Gly Asp Glu His Ile Lys Ala
Glu Tyr Val Ala Ser Leu Ile Arg Ser Val Tyr Glu Pro Ile
Leu Ala Ser His Phe Gly Glu Ala Ile Met Pro Asp Leu Phe
His Arg Leu Ala Lys His Ala Ala Lys Val Leu His Leu Gly

14

28

42

56

70

84

98

112

126

140

154

168

182

196

210

224

238

252

266

280

294

308

322

336

350

364

delete

re-number
Correctly

Please ensure that all nucleotides
and amino acids are valid.

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.